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AM nucleic - nucleic search, using sw model

Run on: February 28, 2001, 10:35:20 ; Search time 54.23 Seconds
(without alignments)
1836.568 Million cell updates/sec

Title: US-09-352-570-1
Perfect score: 618
Sequence: 1 atggcgctgcagctctccg.....aaattcctgtaagtactga 618

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	618	100.0	618	2	US-08-684-024-3
2	618	100.0	618	3	US-09-145-868-3
3	618	100.0	1484	2	US-08-684-024-5
4	618	100.0	1484	3	US-09-145-868-5
5	82.2	13.3	591	2	US-08-684-024-4
6	82.2	13.3	591	3	US-09-145-868-4
7	35.8	5.8	7218	1	US-08-232-463-14
8	32.2	5.2	2694	1	US-08-465-995A-3
9	32.2	5.2	2694	2	US-08-465-994C-3
10	32.2	5.2	2694	2	US-08-966-145-3
11	32.2	5.2	2760	1	US-08-101-593-3
12	30.8	5.0	615	3	US-08-842-807A-22
13	30.6	5.0	4500	2	US-08-743-637B-35
14	30.6	5.0	4500	3	US-08-526-840B-35
15	30.2	4.9	1659	3	US-09-083-351-3
16	30.2	4.9	1959	3	US-09-166-460-1
17	30.2	4.9	3946	3	US-09-083-351-1
18	30	4.9	43676	3	US-09-356-952-12
19	29.8	4.8	1060	1	US-08-850-118-1
20	29.8	4.8	1060	2	US-09-008-253-1
21	29.8	4.8	1060	3	US-09-093-335-1
22	29.6	4.8	5578	1	US-08-081-610-2
23	29.4	4.8	1194	3	US-08-929-329-3
24	29.2	4.7	1130	1	US-07-864-004B-1
25	29.2	4.7	1130	1	US-08-251-937A-1
26	29.2	4.7	1130	1	US-08-212-133A-5
27	29.2	4.7	1130	1	US-08-474-503-3
28	29.2	4.7	1130	2	US-08-670-707A-3

29 29.2 4.7 1130 4 PCT-US93-03275-1 Sequence 1, Appli
30 29.2 4.7 1130 4 PCT-US94-13200-3 Sequence 3, Appli
31 29.2 4.7 1425 1 US-07-715-184-3 Sequence 3, Appli
32 29.2 4.7 1425 1 US-07-876-280-6 Sequence 6, Appli
33 29.2 4.7 1425 1 US-07-876-280-27 Sequence 27, Appli
34 29.2 4.7 1425 1 US-07-935-310A-1 Sequence 1, Appli
35 29.2 4.7 1425 1 US-07-828-788A-1 Sequence 1, Appli
36 29.2 4.7 1425 1 US-08-049-783-3 Sequence 3, Appli
37 29.2 4.7 1425 1 US-08-147-189-1 Sequence 1, Appli
38 29.2 4.7 1425 1 US-08-316-301A-7 Sequence 7, Appli
39 29.2 4.7 1425 2 US-08-904-278-1 Sequence 1, Appli
40 29.2 4.7 1425 3 US-09-076-137-7 Sequence 7, Appli
41 29.2 4.7 1425 4 PCT-US92-03624-7 Sequence 7, Appli
42 29.2 4.7 1425 4 PCT-US92-11337-1 Sequence 1, Appli
43 29.2 4.7 1425 4 PCT-US93-07409-1 Sequence 1, Appli
44 29.2 4.7 1623 1 US-08-121-202-3 Sequence 3, Appli
45 29.2 4.7 2599 5 5266464-1 Patent No. 5266464

ALIGNMENTS

RESULT 1
US-08-684-024-3
Sequence 3, Application US/08684024
Patent No. 5834298
GENERAL INFORMATION:
APPLICANT: Benezza, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-684-024-3

Query Match 100.0%; Score 618; DB 2; Length 618;
Best Local Similarity 100.0%; Pred. No. 1.7e-192;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggcgctgcagctctccgagaggaggaatcacccctgcgcggggagccgcgaatactctg 60
Db 1 ATGGCGCTGCAGCTCTCCCGGGAGGAGGAATCACCCCTGCGGGAGCGCCGAATCGTG 60
QY 61 gccgagttcttcattcggcatcaacacatttatcagctggtgcataatccatct 120


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684.024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..648
US-08-684-024-5

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Query Match 100.0%; Score 618; DB 2; Length 1484;
Best Local Similarity 100.0%; Pred. No. 2.8e-192;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 atggcgctgcagctctccgggagcagggaatcaacctgcgcgggagcgcaaatcgtg 60
3b 34 ATGGCGCTGCAGCTCTCCGGGAGCAGGGAATCAACCTGCgcgggagcgcaaatcgtg 93
2y 61 gccgagttctctcattcggcatcaacagcattttatcatcagcgtggcatatccatct 120
3b 94 GCCGAGTCTCTCATTCCGGCATCAACAGCAATTTATATCAGCGTGGCATATCCATCT 153
2y 121 gaaacctttactcagtgacagaaatcaggaactcaacctgcttgtaactactgattgag 180
3b 154 GAAACCTTTACTCGAGTGCAGAAATACGAGCTCACTTGTGTAAGTACTGATCTTGAG 213
2y 181 ctcaataaatacctaaataatgtgtgaacaaactgaagattgtttatacaagtttca 240
3b 214 CTCATAAAATACCTAAATAATGTGTGGAACAACTGAAAGATTGTTATACAAAGTTTCA 273
2y 241 gttcagaactggttgtagttatctcaaatattgaaagtggtaggtctctggaagatgg 300
3b 274 GTTCAGAAACTGGTGTAGTTATCTCAATATTGAAAGTGGTAGGTCTCGAAAGATGG 333
2y 301 cagtttgattgagtgacaaagactgcaaaagatgacagtgcacccagagaaagtct 360
3b 334 CAGTTTGATTGAGTGTGACAAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCT 393
2y 361 cagaagctatccagatgaatccgttcagtgatcacagatcacagctacggtgaca 420
3b 394 CAGAAGCTATCCAGATGAATCCGTTGAGTGATCAGAGATCACAGATCACAGTACAGT 453
2y 421 ttctgcacactgttggaagtctctgttcatttgatctcgtgatttatcacagaaagt 480
3b 454 TTCTGCCACAGTGTGGAGTTCTTGTTCATTGTTGATCTGCTGATTATACAGACAAAGAT 513
2y 481 ttggttgactgaaataatgggaagctggaagctggaacacagttttaccacattctgagaa 540
3b 514 TTGGTTGTACCTGAAAAATGGGAAGAGTGGGACCAACAGTATTATACCAATTTCTGAGAA 573
2y 541 gtgcctctgcttactactactcaatccaaagtaaatagatggtgacctacaaa 600
3b 574 GTGCCCTCTGCTCAATTTACTACTACTCAATCCAAAGTAATAGCATGCTGGCCCTACAAA 633
2y 601 attcctgcaatgactga 618
3b 601 attcctgcaatgactga 618

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Db 634 ATTCTGTCAATGACTGA 651
RESULT 4
US-09-145-868-5
Sequence 5, Application US/09145868
Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Benezia, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,868
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..648
US-09-145-868-5

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Query Match 100.0%; Score 618; DB 3; Length 1484;
Best Local Similarity 100.0%; Pred. No. 2.8e-192;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atggcgctgcagctctccgggagcagggaatcaacctgcgcgggagcgcaaatcgtg 60
Db 34 ATGGCGCTGCAGCTCTCCGGGAGCAGGGAATCAACCTGCgcgggagcgcaaatcgtg 93
Qy 61 gccgagttctctcattcggcatcaacagcattttatcatcagcgtggcatatccatct 120
Db 94 GCCGAGTCTCTCATTCCGGCATCAACAGCAATTTATATCAGCGTGGCATATCCATCT 153
Qy 121 gaaacctttactcagtgacagaaatcaggaactcaacctgcttgtaactactgattgag 180
Db 154 GAAACCTTTACTCGAGTGCAGAAATACGAGCTCACTTGTGTAAGTACTGATCTTGAG 213
Qy 181 ctcaataaatacctaaataatgtgtggaacaaactgaagattggtttatacaagtttca 240
Db 214 CTCATAAAATACCTAAATAATGTGTGGAACAACTGAAAGATTGTTATACAAAGTTTCA 273
Qy 241 gttcagaactggttgtagttatctcaaatattgaaagtggtaggtctctggaagatgg 300
Db 274 GTTCAGAAACTGGTGTAGTTATCTCAATATTGAAAGTGGTAGGTCTCGAAAGATGG 333
Qy 301 cagtttgattgagtgacaaagactgcaaaagatgacagtgcacccagagaaagtct 360

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MOLECULE TYPE: DNA (genomic)
US-09-145-868-4

Query Match 13.3%; Score 82.2; DB 3; Length 591;
Best Local Similarity 49.5%; Pred. No. 2.1e-17;
Matches 272; Conservative 0; Mismatches 268; Indels 9; Gaps 2;

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2Y 58 gtggcagagttcttctcattcgtgacacacagcattttatatacagcgtggcatatataca 117
Db 40 GTACAGAAATTTTTCAGTACAGCAATTAATTCATTTTGTACCAAGAGCGGTATACCCA 99
QY 118 tctgaacaccttactcagtgagagaatacgcactcacccttcttgtaactactatctt 177
Db 100 GCAGAGATTTTCGTACGGTGAAGAGTAGATCTTACGTTACTTAAGACACATGATGAT 159
QY 178 gagctcaataaacctcaataatgtggtgggaacactgaagagattggtttatatacagtg 237
Db 160 GAACTGAAAGATTACATTCGGAAATTCCTACAAAGTTACAGGTTGGCTTCTTGGTGGA 219
QY 238 tcagttcagaacactggttgtagttatctcaaatattgaagtgtgagtccttggaaga 297
Db 220 AATGCAATCAATTAGTATATATATATATATATATATATATATATATATATATATAT 279
QY 298 tggcagttgatattgagtgacagagactgcaaaagatgacagtgccccagagaaaag 357
Db 280 TGTGCTT---CAATGTGCAACACATTTCTGGCAATAGCAAGGGCAGGATGATGTTGTA 336
QY 358 tctcagaagctatccagagatgaataatccgttcagtgatcagacagatcacagtcagtg 417
Db 337 GATTTAAATACACACAAATCACAATCAGAGCTTTAATCAGGCAAAATCACCTCAAGCGTT 396
QY 418 acatttctgcc-----actgttggaagttcttcttcttcttcttcttcttcttcttataca 471
Db 397 ACCTTCTCCCGAACTACAAAGAGTGGGTACACATTCACAGTACTTGCATATACA 456
QY 472 gacaaagatttggtgtactgaaataatgggaagagtcgggaccacagttttattaccaat 531
Db 457 GACGGGATGCTTAAGTTCGGTTAGATGGCGGACATCCAAATAGTAAAGATACCTGAT 516
QY 532 tctgaggaagtgcccttgcttcttactactatacacaatacacaataatagcagtggtg 591
Db 517 GGTGAAGTAGTCAATTAACAAATCTCTACCAAGCATCATAAAGTTGGTGGCAGGTC 576
QY 592 gactacaaa 600
Db 577 AGCTATAAA 585
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RESULT 7
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463

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; FILING DATE: -  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZgpt-Fls  
US-08-232-463-14  
  
Query Match 5.8%; Score 35.8; DB 1; Length 7218;  
Best Local Similarity 7.5%; Pred. No. 0.12;  
Matches 19; Conservative 132; Mismatches 104; Indels 0; Gaps 0;  
  
QY 186 aaatacctcaataatggtggaacactgaagattggtttatatacagtggttcagttca 245  
Db 1283 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1224  
QY 246 gaaactggttgtagttatctcaaatattgaaagtgtgagtccttggaagatggcagtt 305  
Db 1223 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1164  
QY 306 tgatattgagtgacagactgcaaaagatgacagtgccccagagaaaagtctcagaa 365  
Db 1163 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1104  
QY 366 agctatcagagatgaatccggttcagtcagatcacagatcacagtcagtgacatttct 425  
Db 1103 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 425  
QY 426 gccactgttggaagt 440  
Db 1043 GCCAAGCTCGGAATT 1029
```

RESULT 8
US-08-465-995A-3
Sequence 3, Application US/08465995A
Patent No. 5660980
GENERAL INFORMATION:
APPLICANT: Myron F. Goodman
APPLICANT: Linda J. Rena-Krantz
TITLE OF INVENTION: METHODS FOR IDENTIFYING AND ISOLATING
TITLE OF INVENTION: VARIANT T4 POLYMERASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson, LLP
STREET: 201 No. 5660980th Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: ASCII DOS/TEXT
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,995A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robert Berlinger
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 1920-305D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/977-1001
TELEFAX: 213/977-1003
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE: CDS
LOCATION: 1..2694
US-08-465-995A-3

Query Match 5.2%; Score 32.2; DB 1; Length 2694;
Best Local Similarity 49.1%; Pred. No. 1.1;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Y 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaaa 233
b 1291 TTTAAAGTTTCATCCATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350
Y 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctcgga 293
b 1351 TATTCCTGTTCTCCGAATGGATGTATGATAAATCATCAAGAGGTATCATTCCTCAAG 1410
Y 294 aagatggcagttgtattgtgtgcaagactgcaaaagatgacagtgac 346
b 1411 GAATCGCTAAAGTATTTTCCACCGTAAGACTGGAAAAAGAAATGTTTCGC 1463

RESULT 9

US-08-465-994C-3
Sequence 3, Application US/08465994C
Patent No. 5928919

GENERAL INFORMATION:
APPLICANT: MYRON F. GOODMAN
APPLICANT: LINDA L. REHA-KRANTZ
TITLE OF INVENTION: VARIANT DNA POLYMERASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berlinger & Carson, LLP
STREET: 201 No. 5928919th Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California

COUNTRY: USA

ZIP: 90012-2628

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: ASCII DOS/TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,994C

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MARGARET A. CHURCHILL

REGISTRATION NUMBER: 39,944

REFERENCE/DOCKET NUMBER: 1920-305D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 213/977-1001

TELEFAX: 213/977-1003

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2694 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE: CDS
LOCATION: 1..2694
US-08-465-994C-3

Query Match 5.2%; Score 32.2; DB 2; Length 2694;
Best Local Similarity 49.1%; Pred. No. 1.1;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaaa 233
Db 1291 TTTAAAGTTTCATCCATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350
QY 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctcgga 293
Db 1351 TATTCCTGTTCTCCGAATGGATGTATGATAAATCATCAAGAGGTATCATTCCTCAAG 1410
QY 294 aagatggcagttgtattgtgtgcaagactgcaaaagatgacagtgac 346
Db 1411 GAATCGCTAAAGTATTTTCCACCGTAAGACTGGAAAAAGAAATGTTTCGC 1463

RESULT 10

US-08-966-145-3
Sequence 3, Application US/08966145A
Patent No. 5945312

GENERAL INFORMATION:
APPLICANT: Goodman, Myron F.
APPLICANT: Reha-Krantz, Linda J.
TITLE OF INVENTION: Synthesis of Fluorophore-Labeled DNA
FILE REFERENCE: 1920-353D1
CURRENT APPLICATION NUMBER: US/08/966,145A
EARLIER FILING DATE: 1997-11-07
EARLIER FILING DATE: 1996-04-15
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3

LENGTH: 2694 base pairs

TYPE: DNA

ORGANISM: T4 bacteriophage

PUBLICATION INFORMATION:

AUTHORS: Goodman, Myron F.

AUTHORS: Reha-Krantz, Linda J.

PATENT DOCUMENT NUMBER: US 5,660,980

PATENT FILING DATE: 1995-06-06

PUBLICATION DATE: 1997-08-26

US-08-966-145-3

Query Match 5.2%; Score 32.2; DB 2; Length 2694;

Best Local Similarity 49.1%; Pred. No. 1.1;

Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 174 tcttgagctcataaaatacctaaataatgtgtggaacaactgaaagattggtatacaaa 233
Db 1291 TTTAAAGTTTCATCCATTCATGAATATATCGCAGGAACAGCTCTAAACCGAGTGATGAA 1350
QY 234 gtgttcagttcagaactgtgttagttatctcaaatattgaaagtgtgagtcctcgga 293
Db 1351 TATTCCTGTTCTCCGAATGGATGTATGATAAATCATCAAGAGGTATCATTCCTCAAG 1410
QY 294 aagatggcagttgtattgtgtgcaagactgcaaaagatgacagtgac 346
Db 1411 GAATCGCTAAAGTATTTTCCACCGTAAGACTGGAAAAAGAAATGTTTCGC 1463

RESULT 11

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743.637B
FILING DATE: 04-NOV-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526.840

FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012

TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 4500 base pairs

TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ORGANISM: Streptococcus pneumoniae

US-08-743-637B-35

Query Match 5.0%; Score 30.6; DB 2; Length 4500;
Best Local Similarity 50.3%; Pred. No. 4.6;

Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

161 ttgtaactactgctgagctcataaaatcacctaaataatgtgtggaacaactgaaag 220

1688 TTCAGTTCTTTAGTTATCTAGTTCACCTGATGATCAACTCTCTGACCATTTGAAGC 1629

221 attggttatacaagtggttcagtcagaaactggttagttatctcaaatattgaaagt 280

1628 ATTGTTTCAACATCTCTTTTCTATCACTGTTTCGACATTTTCCAAATCTCGTGCATA 1569

281 gtgaggtctctggaagatgagcagttgat 309

1568 GTAATCTCTTGGAAATTTTCTTCTTCTGCT 1540

RESULT 14

US-08-526-840B-35/c

Sequence 35, Application US/08526840B

Patent No. 6001564

GENERAL INFORMATION:

APPLICANT: BERGERON, Michel G.

APPLICANT: OUELLETTE, Marc

APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND

TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES

TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...

NUMBER OF SEQUENCES: 177

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: USA

ZIP: 53202-4497

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/526.840B

FILING DATE: 11-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/526.840

FILING DATE: 11-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 850586.90012

TELEPHONE: (414) 277-5000

TELEFAX: (414) 277-5591

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 4500 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORGANISM: Streptococcus pneumoniae

US-08-743-637B-35

Query Match 5.0%; Score 30.6; DB 2; Length 4500;
Best Local Similarity 50.3%; Pred. No. 4.6;

Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

161 ttgtaactactgctgagctcataaaatcacctaaataatgtgtggaacaactgaaag 220

1688 TTCAGTTCTTTAGTTATCTAGTTCACCTGATGATCAACTCTCTGACCATTTGAAGC 1629

221 attggttatacaagtggttcagtcagaaactggttagttatctcaaatattgaaagt 280

1628 ATTGTTTCAACATCTCTTTTCTATCACTGTTTCGACATTTTCCAAATCTCGTGCATA 1569

281 gtgaggtctctggaagatgagcagttgat 309

1568 GTAATCTCTTGGAAATTTTCTTCTTCTGCT 1540

RESULT 15

US-09-083-351-3

Sequence 3, Application US/09083351

Patent No. 6087107

GENERAL INFORMATION:

APPLICANT: Sheffield, Val C.

APPLICANT: Alward, Wallace L.M.

APPLICANT: Stone, Edwin M.

APPLICANT: Nishimura, Darryl

APPLICANT: Patil, Shiva

TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS FOR

TITLE OF INVENTION: CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN

TITLE OF INVENTION: TRANSCRIPTION FACTOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/083,351

FILING DATE: 22-MAY-1998

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: UIA-029.02

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1659 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-083-351-3

Query Match 4.9%; Score 30.2; DB 3; Length 1659;
 Best Local Similarity 58.2%; Pred. No. 3.6; Indels 0; Gaps 0;
 Matches 53; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 27 1 atggcgctcagctctcccgaggagcagggaatcacccctgcggggagcgccgaaatcgtg 60
 25 265 ATGGCCATCCAGAACGCCCGGACAGAGATCACCCCTGACGGGCATCTACCGTTCATC 324
 27 61 gcgagttcttcttcattcgccatcaacagca 91
 25 325 ATGGACCGCTTCCCTTCTACCGGGACAACA 355

Search completed: February 28, 2001, 16:02:04
 Job time: 19604 sec

3 BLANK (c)

THIS PAGE BLANK (c) (SPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2001, 15:00:31 ; Search time 11.92 seconds
(without alignments)
299,786 Million cell updates/sec

Title: US-09-352-570-2
Perfect score: 1010
Sequence: 1 REQGITLRGSAIEVAEFFSF.....FTTIHKVNSMVAIKIPVND 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1010	100.0	205	2	US-08-684-024-1
2	1010	100.0	205	2	US-08-684-024-7
3	1010	100.0	205	3	US-09-145-868-1
4	1010	100.0	205	3	US-09-145-868-7
5	1003	99.3	205	2	US-08-684-024-6
6	1003	99.3	205	3	US-09-145-868-6
7	804.5	79.7	203	2	US-08-684-024-8
8	804.5	79.7	203	3	US-09-145-868-8
9	395.5	39.2	196	2	US-08-684-024-2
10	395.5	39.2	196	2	US-08-684-024-9
11	395.5	39.2	196	2	US-09-145-868-2
12	395.5	39.2	196	3	US-09-145-868-9
13	74	7.3	392	3	US-08-979-917A-2
14	72.5	7.2	418	1	US-08-261-206A-72
15	72.5	7.2	565	3	US-09-139-424-3
16	72	7.1	433	2	US-09-139-424-4
17	72	7.1	433	3	US-08-706-216-4
18	71	7.0	2233	2	US-08-569-853-1
19	71	7.0	2233	2	US-08-569-853-2
20	71	7.0	2233	3	US-08-987-439-1
21	70.5	7.0	182	3	US-08-691-563C-90
22	70.5	7.0	624	2	US-08-642-406A-22
23	70.5	7.0	773	3	US-08-434-000A-2
24	70	6.9	689	1	US-08-248-021A-2
25	69.5	6.9	1089	1	US-08-180-195-36
26	69.5	6.9	1089	1	US-08-477-329-36
27	69.5	6.9	1089	2	US-08-475-458-36
28	69.5	6.9	1089	3	US-08-980-400-36

29 68.5 6.8 215 2 US-08-935-396-10 Sequence 10, Appl
30 68.5 6.8 378 2 US-08-986-217-6 Sequence 6, Appl
31 68.5 6.8 380 2 US-09-028-587-4 Sequence 4, Appl
32 68.5 6.8 380 2 US-09-227-420-4 Sequence 4, Appl
33 68.5 6.8 539 3 US-08-941-445A-21 Sequence 13, Appl
34 68.5 6.8 583 3 US-08-941-445A-13 Sequence 21, Appl
35 68.5 6.8 593 2 US-08-987-466-1 Sequence 1, Appl
36 68 6.7 431 2 US-08-928-613-2 Sequence 2, Appl
37 68 6.7 431 3 US-09-193-524-2 Sequence 2, Appl
38 68 6.7 432 1 US-07-698-926A-2 Sequence 2, Appl
39 68 6.7 634 1 US-07-872-644-51 Sequence 51, Appl
40 68 6.7 634 1 US-08-297-494-51 Sequence 51, Appl
41 68 6.7 634 1 US-08-297-510-51 Sequence 51, Appl
42 68 6.7 634 1 US-08-479-532-51 Sequence 51, Appl
43 68 6.7 634 1 US-08-455-526-51 Sequence 51, Appl
44 68 6.7 634 1 US-08-455-525-51 Sequence 51, Appl
45 68 6.7 634 3 US-09-139-491-51 Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-08-684-024-1
; Sequence 1, Application US/08684024
; Patent No. 5834298
; GENERAL INFORMATION:
; APPLICANT: Benezira, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684:024
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-684-024-1

Query Match 100.0%; Score 1010; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 REQGITLRGSAIEVAEFFSFSGINSILYQGIYPSFTFRVQKYGLTLVTTDLEIKYLN 60
DB 7 REQGITLRGSAIEVAEFFSFSGINSILYQGIYPSFTFRVQKYGLTLVTTDLEIKYLN 66
QY 61 NVVEOLKDWLYKCSYQKLVVWISNIESGVLERWOFDECDKTAKDSDAPREKSOKAIOD 120

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.b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 180
* .b 127 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
.b 187 TTTTHKVNMSVAYKIPVND 205

RESULT 2
US-08-684-024-7
; Sequence 7, Application US/08684024
; Patent No. 5834298
; GENERAL INFORMATION:
; APPLICANT: Benzeta, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,024
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; S-08-684-024-7

Query Match 100.0%; Score 1010; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y 1 REQITLGRSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGTLTLVTTDLELIKYN 60
.b 7 REQITLGRSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGTLTLVTTDLELIKYN 66
y 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
.b 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
y 121 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 180
.b 127 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 186
y 181 TTTTHKVNMSVAYKIPVND 199
.b 187 TTTTHKVNMSVAYKIPVND 205
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```
RESULT 3
US-09-145-868-1
; Sequence 1, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Benzeta, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,868
; FILING DATE: 02-SEP-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-145-868-1

Query Match 100.0%; Score 1010; DB 3; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.6e-107;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REQITLGRSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGTLTLVTTDLELIKYN 60
Db 7 REQITLGRSAEIVAEFFSGINSILYQGIYPSSETFTRVQKYGTLTLVTTDLELIKYN 66
Qy 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
Db 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
Qy 121 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 180
Db 127 EIRSVIRQITATVTFPLPVEVSCFDLLIYTDKDLVPEKWEESGPQFITNSEEVRLRSF 186
Qy 181 TTTTHKVNMSVAYKIPVND 199
Db 187 TTTTHKVNMSVAYKIPVND 205

RESULT 4
US-09-145-868-7
; Sequence 7, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Benzeta, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Cooper & Dunham LLP
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-145-868-7

Query Match 100.0%; Score 1010; DB 3; Length 205;
Best-Local Similarity 100.0%; Pred. No. 2.6e-107; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;
QY 1 REQGITLRGSAEIVAEFFSGINSILYQGIYPSFTFTRVQYGLTLLVTTDLEIKYLN 60
DB 7 REQGITLRGSAEIVAEFFSGINSILYQGIYPSFTFTRVQYGLTLLVTTDLEIKYLN 66
QY 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 120
DB 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 126
QY 121 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTNSEEVRRLRSF 180
DB 127 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTNSEEVRRLRSF 186
QY 181 TTTIHKVNSWYKIPVND 199
DB 187 TTTIHKVNSWYKIPVND 205

RESULT 5
US-09-145-868-7
Sequence 6, Application US/08684024
Patent No. 5834298
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Cooper & Dunham LLP
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-145-868-7

FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-684-024-6

Query Match 99.3%; Score 1003; DB 2; Length 205;
Best-Local Similarity 99.5%; Pred. No. 1.6e-106; Indels 0; Gaps 0;
Matches 198; Conservative 0; Mismatches 1;
QY 1 REQGITLRGSAEIVAEFFSGINSILYQGIYPSFTFTRVQYGLTLLVTTDLEIKYLN 60
DB 7 REQGITLRGSAEIVAEFFSGINSILYQGIYPSFTFTRVQYGLTLLVTTDLEIKYLN 66
QY 61 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 120
DB 67 NVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIOD 126
QY 121 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTNSEEVRRLRSF 180
DB 127 EIRSVIRQITATVTFPLLEVSCFDLLIYTDKLVVPEKWEESGPGQFTNSEEVRRLRSF 186
QY 181 TTTIHKVNSWYKIPVND 199
DB 187 TTTIHKVNSWYKIPVND 205

RESULT 6
US-09-145-868-6
Sequence 6, Application US/09145868
Patent No. 6096522
GENERAL INFORMATION:
APPLICANT: Benezra, Robert
TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: Cooper & Dunham LLP
FILING DATE: 02-SEP-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-684-024-6

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
S-09-145-868-6

Query Match 99.3%; Score 1003; DB 3; Length 205;

Best Local Similarity 99.5%; Pred. No. 1.6e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 REQITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 60
D 7 REQITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 66
Y 61 NVPEQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 120
D 67 NVPEQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQD 126
Y 121 EIRSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 180
D 127 EIRSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSF 186
Y 181 TTIHKVNSWVAYKIPVND 199
D 187 TTIHKVNSWVAYKIPVND 205

RESULT 7

S-08-684-024-8

Sequence 8, Application US/08684024

Patent No. 5834298

GENERAL INFORMATION:

APPLICANT: Beneza, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,024

FILING DATE: 19-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1747/46621-A

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 203 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

S-08-684-024-8

Query Match

Best Local Similarity 79.7%; Score 804.5; DB 2; Length 203;

Matches 158; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

QY 3 QGITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 62

Db 8 EGITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 67
QY 63 VEQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQDEI 122
Db 68 TDQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQDEI 126
QY 123 RSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSFTT 182
Db 127 RSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSFTT 186
QY 183 TTIHKVNSWVAYK 194
Db 187 TTIHKVNSWVAYK 198

RESULT 8

US-09-145-868-8

Sequence 8, Application US/09145868

Patent No. 6096522

GENERAL INFORMATION:

APPLICANT: Beneza, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/145,868

FILING DATE: 02-SEP-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 1747/46621-B

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 203 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-145-868-8

Query Match

Best Local Similarity 79.7%; Score 804.5; DB 3; Length 203;

Matches 158; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

QY 3 QGITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 62
Db 8 EGITLGRSAEIVAEFFSGINSILYQGIYPSFTFTRVQKYGLTLLVTTDLLEIKYLN 67
QY 63 VEQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQDEI 122
Db 68 TDQLKDWLYKCSQKLVVVISNIESGEVLERWQFDIECDKTAKDSDAPREKSQKAIQDEI 126
QY 123 RSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSFTT 182
Db 127 RSVIRQITATVTFPLLEVSCSFDLLIYTDKDLVPEKWEESGPGQFITNSEEVRLRSFTT 186

2Y 183 TIKHNSMAYK 194
Db 187 TIKHNSMAYK 198

RESULT 9

JS-08-684-024-2
; Sequence 2, Application US/08684024

; Patent No. 5834298

; GENERAL INFORMATION:

; APPLICANT: Beneza, Robert

; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/684,024

; FILING DATE: 19-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 1747/46621-A

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 196 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

JS-08-684-024-2

Query Match 39.2%; Score 395.5; DB 2; Length 196;

Best Local Similarity 43.1%; Pred. No. 2.4e-37;

Matches 85; Conservative 37; Mismatches 66; Indels 9; Gaps 3;

2Y 3 QGITLRGSAEIVAEFFSGINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYLNW 62

Db 3 QSISLKGSTRTVTEFFEYSINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYIRKI 62

2Y 63 VEQLKDWLYKCSQKLVVVISNESGEVLERWQFDIE---CDKTAKDDSDAPREKSQKATQ 119

Db 63 LIQVHRWLGGKCNQLVLCVNDKDEGEVVERWFSNVQHISGNSGQDDVV----DLNTTQ 118

2Y 120 DEIRSVIROITATVTLPL--EVSCSFDLLIYTDKLVVPEKWEESGPGQFITNSEEVL 177

Db 119 SQIRALIROITSSVTFPELTKEGGYTFVLTADAKVPLEWADSNKSEIPDGEVVOF 178

2Y 178 RSFTTTHKVNMSVAYK 194

Db 179 KTFSTNDHKVGAQVSYK 195

RESULT 10

JS-08-684-024-9

; Sequence 9, Application US/08684024

; Patent No. 5834298

; GENERAL INFORMATION:

; APPLICANT: Beneza, Robert

; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/684,024

; FILING DATE: 19-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 1747/46621-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0526

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 196 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-684-024-9

Query Match 39.2%; Score 395.5; DB 2; Length 196;

Best Local Similarity 43.1%; Pred. No. 2.4e-37;

Matches 85; Conservative 37; Mismatches 66; Indels 9; Gaps 3;

QY 3 QGITLRGSAEIVAEFFSGINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYLNW 62

Db 3 QSISLKGSTRTVTEFFEYSINSILYQRYGYPSETFTRVQKYGLTLVTTDLLEIKYIRKI 62

QY 63 VEQLKDWLYKCSQKLVVVISNESGEVLERWQFDIE---CDKTAKDDSDAPREKSQKATQ 119

Db 63 LIQVHRWLGGKCNQLVLCVNDKDEGEVVERWFSNVQHISGNSGQDDVV----DLNTTQ 118

QY 120 DEIRSVIROITATVTLPL--EVSCSFDLLIYTDKLVVPEKWEESGPGQFITNSEEVL 177

Db 119 SQIRALIROITSSVTFPELTKEGGYTFVLTADAKVPLEWADSNKSEIPDGEVVOF 178

QY 178 RSFTTTHKVNMSVAYK 194

Db 179 KTFSTNDHKVGAQVSYK 195

RESULT 11

US-09-145-868-2

; Sequence 2, Application US/09145868

; Patent No. 6096522

; GENERAL INFORMATION:

; APPLICANT: Beneza, Robert

; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,604
FILING DATE: 25-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Zitron, Anne E.
REGISTRATION NUMBER: 41,391
REFERENCE/DOCKET NUMBER: 0646/1B917-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6118050e
US-08-979-917A-2

Query Match 7.3%; Score 74; DB 3; Length 392;
Best Local Similarity 19.8%; Pred. No. 2.8;
Matches 48; Conservative 38; Mismatches 77; Indels 80; Gaps 12;
QY 9 GSAEIVAEFF--SFGINSILYQRIYPS--ETFRVQKYGTLTVDLELKLNNVVE 64
DB 27 GNAQAASFFCNKMGFFFLAY-RGLETGSREVSVHVKRGKIVFV-----LCSALNPWK 80
QY 65 QLKDWLYKCSVQKLNVVISNIESGEVLEWFOFIE-CDKTAKDSDAPREKSKAIQ---- 119
DB 81 EMGDHLVK-----GDGVKDIAFEVEDCDHIVQ---KARERCAKIVREPWF 122
QY 120 -----DEIRSVIRQIATVTFPLPLEV-----SCSFDDLII 150
DB 123 EQDKFGKVFALQYGDTHTLVEKINYTGRLPGPEAPYKDTLLPKLPRCNLEIIDH 182
QY 151 -----TDKDLVPEKWEESGPOF-----ITNSEVRLRFTTTHKVNWSVWAKIP 196
DB 183 IVGNQPDQMSQASEWYLNQFHFRFWSVDDTVQHTYSLRSIVVT-----NYEESIKMP 238
QY 197 VND 199
DB 239 INE 241

RESULT 14
US-08-261-206A-72
Sequence 72, Application US/08261206A
Patent No. 5574007
GENERAL INFORMATION:
APPLICANT: Zushi, Mitichitaka
APPLICANT: Gomi, Komakazu
APPLICANT: Yamamoto, Shuji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848

TELEX: 248345
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-206A-72

Query Match 7.2%; Score 72.5; DB 1; Length 418;
Best Local Similarity 32.1%; Pred. No. 4.5;
Matches 27; Conservative 12; Mismatches 36; Indels 9; Gaps 3;
QY 42 KYGLTLLVTTDLELKLNNVVEQLDWLYKCSVQKLNVVISNIESGEV--LERWQFDIE 99
DB 75 KYSLQPVVP---ELEKLLGKSVTFAPD---CVGAEEGIVAKADGGAVVLLNLRPHIE 127
QY 100 CDKTAKDSDAPREKSKAIQIDEIR 123
DB 128 EGSAKDKGCKNTKAKAKVDEFR 151

RESULT 15
US-08-961-083-218
Sequence 218, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 565 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-218
Query Match 7.2%; Score 72.5; DB 3; Length 565;
Best Local Similarity 19.9%; Pred. No. 7;
Matches 34; Conservative 37; Mismatches 69; Indels 31; Gaps 8;
QY 29 RGIYPSFTFRVQKYGTLTVDLELKY----LNNVVEQLDWLYKCSVQKLNVVISN 84

2b 278 KGVYASEPVKQPEVNSEINKLKTALNVDKTELNNTIADAK-----TK 322
2y 85 IESGEVLERWQFDIECDKTAKDDSAPEKSKQAIODEIRSVIRQITATVTFPLPLEVSCS 144
3 323 VKEHYSDRSWQ-NLQTEVTKAEKVA---ANTDAKQSEVNEAVEKLTATIE--KLVELS-E 375
y 145 FDLIYTDKDLVVPKWEESGPGFINTNSEEVRLRSFTTTHK---VNSMV 191
b 376 KPILTLTSTDKKILER-EAVAKYTLENQNKTKIKSITAEKKGEEVINTVV 425

Search completed: February 26, 2001, 15:03:32
Job time: 181 sec

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 Date: Feb 28, 2001 4:00 PM
 About: Results were produced by the GenCore software, version 4.5,
 Copyright (c) 1993-2000 CompuGen Ltd.

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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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Search information block:
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 Query length: 199
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/cgn2_6/ptodata/2/pna/US0975_COMB.seq:US-60-904-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US0977_COMB.seq:US-60-929-776-13432	666.00	1389.32	3.5e-68	43	
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/cgn2_6/ptodata/2/pna/US0981_COMB.seq:US-60-979-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US0983_COMB.seq:US-60-1004-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US0985_COMB.seq:US-60-1029-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US0987_COMB.seq:US-60-1054-776-13432	666.00	1389.32	3.5e-68	43	
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/cgn2_6/ptodata/2/pna/US1001_COMB.seq:US-60-1229-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US1003_COMB.seq:US-60-1254-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US1005_COMB.seq:US-60-1279-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US1007_COMB.seq:US-60-1304-776-13432	666.00	1389.32	3.5e-68	43	
/cgn2_6/ptodata/2/pna/US1009_COMB.seq:US-60-1329-776-13432	666.00	1389.32	3.5e-68	43	
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/cgn2_6/ptodata/2/pna/US1141_COMB.seq:US-60-2979-776-13432	666.00	1389.32	3.5e-68	43	
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/cgn2_6/ptodata/2/pna/US1145_COMB.seq:US-60-3029-776-13432	666.00	1389.32	3.5e-68	43	
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167 nPheLeuThrAsnSerGluValArgLeuValArgSerPheThrThrI 184
519 GTTTATTACCAATCTGAGGAAGTCGGCTTCGTTTCATTACTACTACA 568
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seq_documentation_block:
; Sequence 24154, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Polynucleotide Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 24154
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 199471.2
S-60-172-360-24154
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Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
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210 CGGAGCAGGGAATCACCCTCGCGGGAGCCCGGAAATCGTGGCCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProS 34
260 CTCTCATTCGTCATCAACAGCAATTTATATACAGCGTGCATATATCCAT 309
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
310 CTGAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGTGTAAC 359
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
360 ACTGATCTTGAGCTCATAAATACCTAATATGTTGGTGGAACTACTGA 409
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
410 AGATTGGTTATACAGTCTTCAGTTCAGAACTGGTTCTAGTATCTCAA 459
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
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510 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 559
117 aileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValT 134
560 TATCCAGATGAATCCGTCAGTGATCAGACATCACAGCTACGGTGA 609
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
610 CATTCTGCCACTGTGGAAGTTTCTGTTTCATTGATCTGCTGATTAT 659
151 ThrAspLysAspLeuValProGluLysTrpGluSerGlyProG1 167
660 ACAGACAAAGATTGTTGTACCTGAAATAATGGGAAGATCGGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
710 GTTTATTACCAATTCGAGGAAGTCGGCTTCGTTTCATTACTACTACA 759
184 LeHisLysValAsnSerMetValAlaValLysIleProValAsnAsp 199
760 TCCACAAAGTAATAGCATGTGGCTACAAAATTCCTGTCATGAC 806
seq_name: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:US-60-195-106-210
seq_documentation_block:
; Sequence 210, Application US/60195106
; GENERAL INFORMATION:
; APPLICANT: Shiffman, Dov
; APPLICANT: Somogyi, Roland
; APPLICANT: Lawn, Richard M.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Porter, Gordon J.
; APPLICANT: Mikita, Thomas
; APPLICANT: Tai, Julie T.N.
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 P
; CURRENT APPLICATION NUMBER: US/60/195,106
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 210
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 199471.2
US-60-195-106-210
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Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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210 CGGAGCAGGGAATCACCCTCGCGGGAGCCCGGAAATCGTGGCCGAGTT 259
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProS 34
260 CTCTCATTCGTCATCAACAGCAATTTATATACAGCGTGCATATATCCAT 309
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
310 CTGAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGTGTAAC 359
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410 AGATTGGTTATACAAAGTGTTCAGTTCAGAACTGGTTGTAGTTATCTCAA 459
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84 snlLeGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
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460 ATATTGAAAGTGTGTGAGTCTCTGGAAGATGGCAGTTTGTATATGAGTGT 509
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101 AspLysThrAlaLysAspSerAlaProArgGlnLysSerGlnLysAl 117
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510 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAGC 559
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117 aileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValT 134
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|||||
710 GTTATTACCAATTCAGGAGTCCGCTTCGTTTCATTACTACTACAA 759
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184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
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seq_name: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:us-60-213-359-4179

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seq_documentation_block:
; Sequence 4179, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; TITLE OF INVENTION: Identified thereby
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 4179
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 199471.2
; S-60-213-359-4179
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alignment_scores:
Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-352-570-2 x US-60-213-359-4179
align seg 1/1 to: US-60-213-359-4179 from: 1 to: 1505

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210 CGGAGCAGGGAATCACCTTCGCGGGAGCGCGAAATCGTGGCCGAGTT 259
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17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPros 34
|||||
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34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuLeuValThr 50
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51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLys 67
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; Sequence 155, Application US/60238331
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/60/238,331
; CURRENT FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 155
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 199471.2
; US-60-238-331-155
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Ratio: 5.075 Gaps: 0

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17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
260 CTTCTCATTCGCGATCAACAGCATTTTATATCAGCGTGCATATATCAT 309
34 exGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
310 CTGAAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTGTAACT 359
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
360 ACTGATCTTGAGCTCATATAAATACCTAAATATGTTGGTGAACAAC 409
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
410 AGATTGGTTATACAGTGTTCAGTTCAGAAACTGGTTGATTTACTCAA 459
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
460 ATATTGAAAGTGGTGGAGTCTCGGAAAGATGCGAGTTTCATATTGAGTGT 509
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
510 GACAGACTGCAAAAGATACAGTGCACCCAGAGAAAGTCTCAGAAAGC 559
117 alIeGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
560 TATCCAGGATGAATCCGTCAGTGATCAGACAGATCAGATCAGGTTCA 609
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuTyr 150
610 CATTTCTGCACCTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 659
151 ThrAspLysAspLeuValProGluLysTrpGluLysGlyProGly 167
660 ACAGACAAGATTGTTGTTACTGAAATGGAAGATCGGAGATCGGACCACA 709
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrThr 184
710 GTTTATTACCAATTCAGGAAAGTCCGCTTCGTTCAATTACTACTACAA 759
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
760 TCCAAAGTAAATAGCATGTTGGCTGACAAAATTCCTGTCATGATGAC 806
eq_name: /cgn2_5/ptodata/2/pna/US096B_COMB.seq:US-09-693-036-3

eq_documentation_block:
Sequence 3, Application US/09693036
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Yang, Yonghong
APPLICANT: Zhao, Qing A.
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Zhang, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
POLYPEPTIDES
FILE REFERENCE: 784CIP2E

CURRENT APPLICATION NUMBER: US/09/693,036
CURRENT FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 3
LENGTH: 2131
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (104)..(733)
US-09-693-036-3
alignment_scores:
Quality: 1010.00 Length: 199
Ratio: 5.075 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-352-570-2 x US-09-693-036-3/rev ..
Align seg 1/1 to reverse of: US-09-693-036-3 from: 1 to: 2131
1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
2080 CGGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGGCGGAGTT 2031
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
2030 CTTCTCATTCGCGATCAACAGCATTTTATATCAGCGTGCATATATCAT 1981
34 exGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
1980 CTGAAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTGTAACT 1931
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
1930 ACTGATCTTGAGCTCATATAAATACCTAAATATGTTGGTGAACAAC 1881
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
1880 AGATTGGTTATACAGTGTTCAGTTCAGAAACTGGTTGATTTACTCAA 1831
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
1830 ATATTGAAAGTGGTGGAGTCTCGGAAAGATGCGAGTTTGATATTGAGTGT 1781
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
1780 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 1731
117 alIeGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
1730 TATCCAGGATGAATCCGCTCAGTGATCAGACAGATCAGATCAGGTTGA 1681
134 hrPheLeuProLeuGluValSerCysSerPheAspLeuLeuTyr 150
1680 CATTTCTGCACCTGTGGAGTTTCTTGTTCATTTGATCTGCTGATTAT 1631
151 ThrAspLysAspLeuValProGluLysTrpGluLysSerGlyProGly 167
1630 ACAGACAAGATTGTTGTTACTGAAATGGAAGATCGGAGATCGGACCACA 1581
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrThr 184
1580 GTTTATTACCAATTCAGGAAAGTGGCTTCGTTCAATTACTACTACAA 1531
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199

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|||||
1530 TCACAAAGTAATACATGGTGGCCCTACAAAATTCTGTCATGAC 1484

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-352-570-3
seq_documentation_block:
; Sequence 3, Application US/09352570
; GENERAL INFORMATION:
; APPLICANT: Michael E. Mendelsohn
; TITLE OF INVENTION: METHOD FOR ASSAYING COMPOUNDS AFFECTING
; FILE OF INVENTION: CELL DIVISION
; CURRENT APPLICATION NUMBER: 00398/506001
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Ovis aries
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(600)
; 3-09-352-570-3

alignment_scores:
  Quality: 991.00      Length: 199
  Ratio: 5.005        Gaps: 0
  Percent Similarity: 99.497  Percent Identity: 97.990

alignment_block:
US-09-352-570-2 x US-09-352-570-3

Align seg 1/1 to: US-09-352-570-3 from: 1 to: 600

1  ArgGluGlnGlyLeuThrLeuArgGlySerAlaGluLeuValAlaGluPh 17
|||||
1  CGGGAGCAAGGCATACCTTCGCGGGAGCGCGAGATCGTGGCCGAGTT 50
|||||
17  ePheSerPheGlyLeuAsnSerLeuLeuThrLeuArgGlyLeuThrPro 34
|||||
51  CTCTCTATTGGTATCAACAGTATTTATATCATCGGTGGCATATATCAT 100
|||||
34  erGluThrPheThrArgValGlnLysThrGlyLeuThrLeuValThr 50
|||||
101  CGAAACCTTTACTCGAGTCAGAAATATGAGTACCTTCCTTGTAACT 150
|||||
51  ThrAspLeuGluLeuLeuLysThrLeuAsnValValGluGlnLeuLy 67
|||||
151  ACTGATCCTGAGCTCATAAATACCTTAATAATATGTTGGTGGATCACTAA 200
|||||
67  sAspTrpLeuThrLysCysSerValGlnLysLeuValValLysSerA 84
|||||
201  AGAATGGTTATCAAGGTTCAGTTCAGAAACTGGTGTAGTCACTCAA 250
|||||
84  snleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
|||||
251  ATATTGAAAGTCGAGAGGTCCTTGAAGATGGCAGTTTGATATGAGTGT 300
|||||
101  AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
|||||
301  GACAAGACTGCAAAAGATGACATGTCACCCAGAGAAAAGTCTCAGAAGC 350
|||||
117  alleGlnAspLleuArgSerValIleArgGlnIleThrAlaThrValt 134
|||||
351  TATCCAAGATGAATCGTTTCAGTGTATCAGACAGATCAGAGTACAGTAA 400
|||||
134  hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuThr 150
|||||
401  CATTTCTGCCACGTGTGGAAGTTTCTTGTTCATTTGATCTCTCTATAT 450
|||||
151  ThrAspLysAspLeuValValProGluLysTrpGluSerGlyProG1 167
```

```
|||||
451  ACAGACAAAGATCTGTTGTACCTGAGAAATGGAGAGTCCGGACCACA 500
|||||
167  nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
|||||
501  GTTCATTACCAATTCCTGAAGAAGTTCGTTCTTCATTCACTACTACAA 550
|||||
184  leHisLysValAsnSerMetValAlaLeuLysIleProValAsnAsp 199
|||||
551  TTCACAAAGTAATAGTAGCTGAGCTACAAAATTCCTGTCATGAC 597
|||||

seq_name: /cgn2_6/ptodata/2/pna/US095B_COMB.seq:US-09-540-229-121335
seq_documentation_block:
; Sequence 121335, Application US/09540229
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleageane, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullahy, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
; FILE REFERENCE: PD-1033 CIP
; CURRENT APPLICATION NUMBER: US/09/540/229
; CURRENT FILING DATE: 2000-03-31
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 193582
; SOFTWARE: PERL Program
; SEQ ID NO 121335
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01238306
US-09-540-229-121335
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alignment_scores:
  Quality: 789.00      Length: 163
  Ratio: 4.931        Gaps: 1
  Percent Similarity: 98.160  Percent Identity: 96.933

alignment_block:
US-09-352-570-2 x US-09-540-229-121335

Align seg 1/1 to: US-09-540-229-121335 from: 1 to: 527

20  PheGlyIleAsnSerIleLeuThrGlnArgGlyLeuThrProSer Glut 36
|||||
39  TTCGGCATCAACAGCATTTATATACGCGTGGCATATATTCATCTTAAAA 88
|||||
36  hrPheThrArgValGlnLysThrGlyLeuThrLeuValThrAsp 52
|||||
89  CTTTATTTCGAGTGCAGAAATACGGACTCACCTTCCTTGTAACTACTGAT 138
|||||
53  LeuGluLeuLysThrLeuAsnValValGluGlnLeuLysAspTr 69
|||||
139  CTTGAGCTCATAAATACCTTAATAATGTGGTGAACAACACTGAAAGATTG 188
|||||
69  pLeuThrLysCysSerValGlnLysLeuValValIleSerAsnIleG 86
|||||
189  GTTATACAAAGTGTTCAGTTCAGAAACTGGTTGTAGTATCTCAATATTG 238
|||||
86  luSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAspLys 102
|||||
239  AAAGTGGTGGAGTCTTGGAAAGATGCGAGTTTCATATTGAGTGTGACAAG 288
|||||
103  ThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaIleG1 119
|||||
289  ACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAGCTATCCA 338
```

119 nAspGluLeuValSerGlyValLeuArgGlnThrAlaThrValThrPheL 136
 339 GGATGAATCCGTCAGTACAGACAGATCACAGTACGCGGTGACATTC 388
 136 euProLeuLeuValSerCysSerPheAspLeuLeuIleThrThrAsp 152
 389 TGCCACTGTGTGAAGTCTCTTCTTCATTGATCTGCTGATTATACAGAC 438
 133 LysAspLeuValProGluLysTrpGluGluSerGlyProGlnPheL 169
 439 AAAGATTGGTTGTACCTGAAATGGAAGAGTGGGACCACTGTTAT 488
 169 eThrAsnSerGluGluValArgLeuArgSerPheThr 181
 489 TACCATTCTGAGGAAGTCGCGCTTCGTTCAATTACT 525

seq_name: /cgn2_6/ptodata/2/pna/US097_COMB.seq:US-09-726-805-585

seq_documentation_block:
 ; Sequence 585, Application US/09726805
 ; GENERAL INFORMATION:
 ; APPLICANT: Gearing, David P.
 ; APPLICANT: Holtzman, Douglas A.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 1600,2017-001
 ; CURRENT APPLICATION NUMBER: US/09/726,805
 ; CURRENT FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/168,140
 ; PRIOR FILING DATE: 1999-11-30
 ; NUMBER OF SEQ ID NOS: 2158
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 585
 ; LENGTH: 607
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(607)
 ; OTHER INFORMATION: n = A,T,C or G
 ; S-09-726-805-585

alignment_scores:
 Quality: 673.00 Length: 160
 Ratio: 4.457 Gaps: 1
 Percent Similarity: 94.375 Percent Identity: 92.500
 alignment_block:
 US-09-352-570-2 x US-09-726-805-585 ..
 Align seg 1/1 to: US-09-726-805-585 from: 1 to: 607

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
 128 CGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGGCGAGT 177
 17 ePheSerPheGlyIleAsnSerIleLeuTyThrGlnArgGlyIleTyProS 34
 178 CTTCTCATCGGCATCAACAGCATTTTATATCAGCGTGCATATATCAT 227
 34 erGluThrPheThrArgValGlnLysTyThrGlyLeuThrLeuValThr 50
 228 CTGAACCTTTACTACGATGAGAGATACGACATCACCTTCCTGTAAT 277
 51 ThrAspLeuGluLeuIleLysTyThrLeuAsnValValGluGlnLeuLy 67
 278 ACTGATCTGAGCTCATAAATACCTAAATAATGTGGTGAACAACTGAA 327
 67 sasTrpLeuTyLysCysSerValGlnLysLeuValValIleSera 84
 328 AGATTGGTTATACAAGTCTCAGTTTCAGAAACTGGTTGTAGTTATCTCAA 377

84 snileGlu.SerGlyGluValLeuGluArgTrpGlnPheAspIleGluCy 100
 378 ATATTGAAAGTGGTGAAGTCTCTGAAAGATGGCAGTTTGATATGAATG 427
 100 sAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysA 117
 428 TGACAAGACTGCNAAAGATGACAGTTGCACCACAGAGA.AAATCTCAGAAAG 476
 117 laileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 133
 477 CTANCCAGGATGAATCCGTTTCAGTGATCAGACAGATCACAGCTACNGGT 526
 134 ThrPheLeuProLeuGluValSerCysSerPheAspLeuIleTy 150
 527 GACTTTCGCCACACTGTGGAATTCCTGTTCAATT.GAICTGCCGAATTA 575
 150 rThrAspLysAspLeuValValProGlu 159
 576 TACANACAAAGATTGGGTGTTCTCTGAA 603

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-235-076-13432

seq_documentation_block:
 ; Sequence 13432, Application US/09235076
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES,
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/235,076
 ; CURRENT FILING DATE: 1999-01-20
 ; NUMBER OF SEQ ID NOS: 38054
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13432
 ; LENGTH: 439
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(439)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-235-076-13432

alignment_scores:
 Quality: 666.00 Length: 133
 Ratio: 5.045 Gaps: 0
 Percent Similarity: 99.248 Percent Identity: 98.496
 alignment_block:
 US-09-352-570-2 x US-09-235-076-13432 ..

Align seg 1/1 to: US-09-235-076-13432 from: 1 to: 439
 35 GluThrPheThrArgValGlnLysTyThrGlyLeuThrLeuValThrTh 51
 39 GAAACCTTACTCGAGGCGAGAAATACGGACTCACCTTGCTGTGAATAC 88
 51 rAspLeuGluLeuIleLysTyThrLeuAsnValValGluGlnLeuLysA 68
 89 TGATCTTGAGCTCAATAAATACCTAAATAAGGTGGTGAACAACTGAAAG 138
 68 sPTpLeuTyLysCysSerValGlnLysLeuValValIleSerAsn 84
 139 ATTGGTTATACAAGTGTTCAGTTCAGAAATCGGTGTAGTTATCTCAAT 188
 85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAs 101
 189 ATTCAAAGTGGTGAAGTCTCTGAAAGATGGCAGTTTGATATGAGTGTA 238
 101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118
 239 CAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAAGCTA 288

118 leGlnaspGluileArgSerValileArgGlnleThrAlaThrValThr 134
 289 TCAGGATGAAATCCGTTTCAGTCATCAGACAGATCACAGTCACGGTGACA 338
 135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrth 151
 339 TTCTGCCACTGTGGAAGTTCTTGTTCATTTGATCTGCTGATTATAC 388
 151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
 389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437

seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-248-797-36033

seq_documentation_block:
 ; Sequence 36033, Application US/09248797
 ; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-764
 ; CURRENT APPLICATION NUMBER: US/09/248,797
 ; CURRENT FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 48909
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 36033
 ; LENGTH: 439

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(439)
 ; OTHER INFORMATION: n = A,T,C or G
 ;S-09-248-797-36033

alignment_scores:
 Quality: 666.00 Length: 133
 Ratio: 5.045 Gaps: 0
 Percent Similarity: 99.248 Percent Identity: 98.496

alignment_block:

US-09-352-570-2 x US-09-248-797-36033

Align seg 1/1 to: US-09-248-797-36033 from: 1 to: 439

35 GluThrPheThrArgValGlnLysTyrglyLeuThrLeuLeuValThr 51
 39 GAAACCTTTACTCGAGGCGAAGTAACGGACTCACCTTGTCTTAACACTAC 88
 51 rAspLeuGluLeuileLysTyrglyLeuAsnValValGluGlnLeuLys 68
 89 TGATCTTGAGCTCATAAATACCTAAATAAGGTGGTGAACAACTGAAAG 138
 68 sPrpLeuTyrglyCysSerValGlnLysLeuValValValIleSerAsn 84
 139 ATTGGTTATACAAGTTTCAGTTCAGAAACTGGTTGATTTATCTCAAT 188
 85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAs 101
 189 ATTGAAAGTGTGAGTCTCGGAAAGATGCGAGTTTGATATTGAGTGTA 238
 101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118
 239 CAAGACTGCAAAAGATGACAGTCACCCAGAGAAAAGTCTCAGAAAAGCTA 288
 118 leGlnAspGluileArgSerValileArgGlnleThrAlaThrValThr 134
 289 TCAGGATGAAATCCGTTTCAGTCATCAGACAGATCACAGTCACGGTGACA 338
 135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrth 151

339 TTCTGCCACTGTGGAAGTTCTTGTTCATTTGATCTGCTGATTATAC 388
 151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
 389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-332-782-13432

seq_documentation_block:
 ; Sequence 13432, Application US/09332782A
 ; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 ; FILE REFERENCE: 20411-756
 ; CURRENT APPLICATION NUMBER: US/09/332,782A
 ; CURRENT FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13432
 ; LENGTH: 439

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(439)
 ; OTHER INFORMATION: n = A,T,C or G
 ;US-09-332-782-13432

alignment_scores:
 Quality: 666.00 Length: 133
 Ratio: 5.045 Gaps: 0
 Percent Similarity: 99.248 Percent Identity: 98.496

alignment_block:

US-09-352-570-2 x US-09-332-782-13432

Align seg 1/1 to: US-09-332-782-13432 from: 1 to: 439

35 GluThrPheThrArgValGlnLysTyrglyLeuThrLeuLeuValThr 51
 39 GAAACCTTTACTCGAGGCGAAGTAACGGACTCACCTTGTCTTAACACTAC 88
 51 rAspLeuGluLeuileLysTyrglyLeuAsnValValGluGlnLeuLys 68
 89 TGATCTTGAGCTCATAAATACCTAAATAAGGTGGTGAACAACTGAAAG 138
 68 sPrpLeuTyrglyCysSerValGlnLysLeuValValValIleSerAsn 84
 139 ATTGGTTATACAAGTTTCAGTTCAGAAACTGGTTGATTTATCTCAAT 188
 85 IleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCysAs 101
 189 ATTGAAAGTGTGAGTCTCGGAAAGATGCGAGTTTGATATTGAGTGTA 238
 101 pLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAlaI 118
 239 CAAGACTGCAAAAGATGACAGTCACCCAGAGAAAAGTCTCAGAAAAGCTA 288
 118 leGlnAspGluileArgSerValileArgGlnleThrAlaThrValThr 134
 289 TCAGGATGAAATCCGTTTCAGTCATCAGACAGATCACAGTCACGGTGACA 338
 135 PheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuileYrth 151
 339 TTCTGCCACTGTGGAAGTTCTTGTTCATTTGATCTGCTGATTATAC 388
 151 rAspLysAspLeuValProGluLysTrpGluGluSerGlyProGln 167
 389 AGACAAAGATTGGTTGTACCTGAAATGGAAGAGTCGGGACCACAG 437

seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-332-782-11844

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eq_documentation_block:
Sequence 11844, Application US/09332782
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-754CON1
CURRENT APPLICATION NUMBER: US/09/332,782
CURRENT FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: US 09/181,430
EARLIER FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 21027
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11844
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
US-09-332-782-11844

alignment_scores:
Quality: 574.00 Length: 116
Ratio: 5.035 Gaps: 0
Percent Similarity: 98.276 Percent Identity: 97.414

alignment_block:
US-09-352-570-2 x US-09-332-782-11844
Align seg 1/1 to: US-09-332-782-11844 from: 1 to: 391
1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
40 CGGGAGCAGGGAATCACCTCGCGGGAGCGCGAAATCGTGCGCGAGTT 89
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
90 CTTCATTCGGCATCACAGCATTTTATATCAGCGTGCATATATCAT 139
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
140 CTGAACCTTTACTCGAGTGCAGAAATACGGACTCACCTTGCTTGA 189
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeu 67
190 ACTGATCTTGAGCTCATAAATACCTAATAATGTGGGGGAACAAC 239
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSera 84
240 AGATTGGTTATACAGTGTTCAGTTCAAAACTGTTGTAGTTATCTCA 289
84 snIleGluSerGlyGluValLeuGluArgTyrGlnPheAspIleGlu 100
290 ATATTGAAAGTGGTGGAGTCTCGGAAAGATGCGAGTGTGATATT 339
101 AspLysThrAlaLysAspSerLysLysLysLysLysLysLysLys 116
340 GACAGACTGCAGAAAGATGACAGTGCACCCAGAGAAAGCTCAGAA 387
eq_name: /cgn2_6/ptodata/2/pna/us0959A_COMB.seq:US-09-515-694-11844

eq_documentation_block:
Sequence 11844, Application US/09515694
GENERAL INFORMATION:
APPLICANT: Arterburn, Matthew
APPLICANT: Asghari, Vida
APPLICANT: Blun, Linda
APPLICANT: Cheung, Patrick
APPLICANT: Damavandi, Simin
APPLICANT: Dickson, Mark
APPLICANT: Drake, Jim
APPLICANT: Engleman, Carrie
```

67 sasptpLeuTyrlLysCysSerValGlnLysLeuValValIleSera 84
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 240 AGATTGGTTATACAGTGTTCAGTTCAAAAGCTGGTGTAGTATCTCAA 289
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 84 snileGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
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 290 ATATTGAAAGTGGTGAAGTCCCTGGAAGATGCGAGTTTGATATTGAGTGT 339
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 101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLys 116
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 340 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGCTCAGAAAG 387
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seq_name: /cgn2_6/ptodata/2/pna/US092_COMB.seq:US-09-235-076-28177

seq_documentation_block:
 : Sequence 28177, Application US/09235076
 : GENERAL INFORMATION:
 : APPLICANT: HYseq, Inc.
 : TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 : TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
 : FILE REFERENCE: 20411-736
 : CURRENT APPLICATION NUMBER: US/09/235.076
 : CURRENT FILING DATE: 1999-01-20
 : NUMBER OF SEQ ID NOS: 38054
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 28177
 : LENGTH: 472
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: misc_feature
 : LOCATION: (1)...(472)
 : OTHER INFORMATION: n = A,T,C or G
 : US-09-235-076-28177

alignment_scores:
 Quality: 572.00 Length: 112
 Ratio: 5.107 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-352-570-2 x US-09-235-076-28177
 Align seg 1/1 to: US-09-235-076-28177 from: 1 to: 472
 1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
 |||||
 135 CGGAGCAGGGAATCACCTGCGGGAGCGCGAAATCGTGGCCGAGTT 184
 |||||
 17 epeSerPheGlyIleAsnSerIleLeuTyrlGlnArgGlyIleTyProS 34
 |||||
 185 CTTCATTCGGCATCAACAGCATTTTATATACAGCGTGCATATATCCAT 234
 |||||
 34 erGluThrPheThrArgValGlnLysTyrlGlyLeuThrLeuValThr 50
 |||||
 235 CTGAACCTTTACTCGAGTGCAGAAATACGAGCTACCTTGTGTAACT 284
 |||||
 51 ThrAspLeuGluLeuIleLysTyrlLeuAsnValValGluGlnLeuLy 67
 |||||
 285 ACTGATCTTGAGCTCATAAAATACCTAAATATGTGTGGTGAACAACTGAA 334
 |||||
 67 sasptpLeuTyrlLysCysSerValGlnLysLeuValValIleSera 84
 |||||
 335 AGATTGGTTATACAGTGTTCAGTTCAGAACTGTTGAGTATCTCAA 384
 |||||
 84 snileGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
 |||||
 385 ATATTGAAAGTGGTGAAGTCCCTGGAAGATGCGAGTTTGATATTGAGTGT 434
 |||||
 101 AspLysThrAlaLysAspSerAlaProArgGlu 112
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435 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAA 470

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67 sasptpLeuTyrLysCysSerValGlnLysLeuValValValIleSera 84
117 AGATTGGTTATACAAAGTGTTCAGTTCAGAAAGTGGTTAGTATCTCAA 268
84 snleGluSerGlyGluValLeuGluArgTyrGlnPheAspIleGluCys 100
269 ATATTGAAAGTGGTGGAGTCCCTGGAAGATGGCAGTTTGATATTGAGTGT 318
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
319 GACAAGACTGCAAAAGATCACAGTGCACCCAGAGAAAGTCTCAGAAAGC 368
117 alleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValt 134
369 TATCCAGGATGAAATTCGTTACCTGAGTATCAGACAGATCAGATCCGGTGA 418
134 hrPheLeuProLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
419 CATTCTGCCACTGTGGAGTTCCTGTTCAATTTGATCTGCTGATTAT 468
151 ThrAspLysAspLeuValValProGluLysTyrGlnPheAspIleGluCys 167
469 ACAGACAAAGATTTGGTTGTTACCTGAAAGTGGCAGAGTCCGGACCACA 518
167 nPheIleThrAsnSerGluValArgLeuArgSerPheThrThrThrI 184
519 GTTTATTACCAATTCAGGAAGTGGCCTTCGTTTCATTACTACTACAA 568
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
569 TCCACAAAGTAAATAGCATGTGGCTTACAAAATTCCTGTCAATGAC 615
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:us-09-145-868-3

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seq_documentation_block:
; Sequence 3, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Beneza, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release.#1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,868
; FILING DATE: 02-SEP-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-B
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; 5'-09-145-868-3
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  Quality: 1010.00      Length: 199
  Ratio: 5.075          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-352-570-2 x US-09-145-868-3 ..
Align seg 1/1 to: US-09-145-868-3 from: 1 to: 618

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
19 CGGGAGCAGGAATCACCTCGCGGGAGCGCCGAAATCGTGGCCGAGTT 68
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
69 CTCTCATTCGCATCACACAGCAATTTATATCAGCGTGGCATATATCCAT 118
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
119 CTGAAACCTTTTACTCGAGTGCAGAAATACGGACTCACCTTCCTGTAAC 168
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
169 ACTGATCTTGAGCTCATATAAATACCTTAATAATGTGGTGGAACTGAA 218
67 sasptpLeuTyrLysCysSerValGlnLysLeuValValValIleSera 84
219 AGATTGGTTATACAAAGTGTTCAGTTCAGAAAGTGGTTAGTATCTCAA 268
84 snleGluSerGlyGluValLeuGluArgTyrGlnPheAspIleGluCys 100
269 ATATTGAAAGTGGTGGAGTCCCTGGAAGATGGCAGTTTGATATTGAGTGT 318
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
319 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 368
117 alleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrValt 134
369 TATCCAGGATGAAATTCGTTACCTGAGTATCAGACAGATCAGATCCGGTGA 418
134 hrPheLeuProLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
419 CATTCTGCCACTGTGGAGTTCCTGTTTCATTTCATTGATCTGCTGATTAT 468
151 ThrAspLysAspLeuValValProGluLysTyrGlnGluSerGlyProGl 167
469 ACAGACAAAGATTTGGTTGTTACCTGAAAGTGGCAGAGTCCGGACCACA 518
167 nPheIleThrAsnSerGluValArgLeuArgSerPheThrThrThrI 184
519 GTTTATTACCAATTCAGGAAGTGGCCTTCGTTTCATTACTACTACAA 568
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
569 TCCACAAAGTAAATAGCATGTGGCTTACAAAATTCCTGTCAATGAC 615

seq_name: /cgn2_6/ptodata/2/ina/5b_COMB.seq:us-08-684-024-5

seq_documentation_block:
; Sequence 5, Application US/08684024
; Patent No. 5834298
; GENERAL INFORMATION:
; APPLICANT: Beneza, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,024
FILING DATE: 19-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/46621-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 34..648
US-08-684-024-5

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alignment_scores:
  Quality: 1010.00      Length: 199
  Ratio: 5.075          Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-352-570-2 x US-08-684-024-5

Align seg 1/1 to: US-08-684-024-5 from: 1 to: 1484

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17
52 CGGAGCAGGAGGAATCACCTCGCGGGAGCCGGAATCGGGCCGAGTT 101
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrPro 34
102 CTTCATTCGGCATCAACAGCATTTTATATACGGTGGCATATATCAT 151
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
152 CTGAACCTTTACTCGAGTCGAGTAACGAGTACGACCTCAGCTTCTGTA 201
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLy 67
202 ACTGATCTTGAGCTCATAAATACCTAAATAATGTGTGGAACTGAA 251
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSerA 84
252 AGATGGTTATACAGTGTTCAGTTCAGAAACTGGTGTAGTTATCTCAA 301
84 snileGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
302 ATATTGAAGTGGTGAGTCTCGTGGAAAGATGGCAGTTTGATATTGAGT 351
101 AspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLysAl 117
352 GACAAGACTGCAAAAGATGACAGTGCACCCAGAGAAAAGTCTCAGAAGC 401
117 aileGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
402 TATCCAGATGAATCCGTTTCAGTGTGATCAGACACATCACAGCTACGGTGA 451

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134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
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452 CATTTCTGCCACTGTGGAAAGTTTCTTTGTTCAATTCATCTGCTGATTAT 501
|||||
151 ThrAspLysAspLeuValValProGluLysTrpGluSerGlyProGlu 167
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502 ACAGACAAAGATTGGTTGTACTGAAAAAAGGAGAGCGGACCA 551
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167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrI 184
|||||
552 GTTATTACCAATTCGAGGAAGTGGCCCTTCATTACTACTACAA 601
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184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
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602 TCCACAAAGTAAATAGCATGTGCGCTACAAAATTCCTGTCATGAC 648
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seq_documentation_block:
; Sequence 5, Application US/09145868
; Patent No. 6096522
; GENERAL INFORMATION:
; APPLICANT: Beneza, Robert
; TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/145,868
; FILING DATE: 02-SEP-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1484 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 34..648
US-09-145-868-5

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  Quality: 1010.00      Length: 199
  Ratio: 5.075          Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-352-570-2 x US-09-145-868-5

Align seg 1/1 to: US-09-145-868-5 from: 1 to: 1484

1 ArgGluGlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPh 17

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52 CGGGAGCAGGGAATCACCCTGCGGGAGCGCGAAATCGTGGCGAGTT 101
17 ePheSerPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProS 34
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102 CTTCTCATTCGCGCATCAACAGCATTTTATATCAGCGTGCATATCCAT 151
34 eGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuValThr 50
|||||
152 CTGAACACTTTACTCGAGTGCAGAAATAGGACTCACCTTGCTTTAACT 201
51 ThrAspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLys 67
202 ACTGATCTGACCTATATAAAATACCTAATATGTGGTGAACACTGAA 251
67 sAspTrpLeuTyrLysCysSerValGlnLysLeuValValIleSera 84
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252 AGATTGGTTATACAAGTGTTCAGTTTCAGAACTGGTTGTAGTTATCTCA 301
84 snIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGluCys 100
302 ATATTGAAAGTGGTGGAGTCTCGAAGATGCGAGTTTGATATTGAGTGT 351
101 AspLysThrAlaLysAspAspSerAlaProArgGluLysSerGlnLysAl 117
352 GACAGACTGCAGAAAGATGACAGTGCACCCAGAGAAAGTCTCAGAAAGC 401
117 aIleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrVal 134
402 TATCAGGATGAATCCGTTTCAGTTCAGTACAGACAGATCAGAGTACGGTGA 451
134 hrPheLeuProLeuLeuGluValSerCysSerPheAspLeuLeuIleTyr 150
452 CATTTCTGCCACTGTGGAGTTCCTTGTTCATTGATCTGCTGATTAT 501
151 ThrAspLysAspLeuValValProGluLysTrpGluGluSerGlyProGl 167
502 ACAGACAAAGATTGTGTTGCTACCTGAAATGGAAGATCGGACACCA 551
167 nPheIleThrAsnSerGluGluValArgLeuArgSerPheThrThrThr 184
552 GTTTATTACCAATCTCGAAGATGCGCCTTCCTTCATTACTACTACAA 601
184 leHisLysValAsnSerMetValAlaTyrLysIleProValAsnAsp 199
602 TCACAAAGTAATAGCATGGTGGCTTACAAAATTCCTGTCAATGAC 648
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eq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-684-024-4

eq_documentation_block:

Sequence 4, Application US/08684024

Patent No. 5834298

GENERAL INFORMATION:

APPLICANT: Benezra, Robert

TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/684,024

FILING DATE: 19-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

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; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1747/46621-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 378-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-684-024-4
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alignment_scores:

Quality: 395.50 Length: 197

Ratio: 2.637 Gaps: 3

Percent Similarity: 76.142 Percent Identity: 43.147

alignment_block:

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Align seg 1/1 to: US-08-684-024-4 from: 1 to: 591

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7 CAATCAATATACATAAGGGTTCAACAGGACAGTATACAGAAATTTTCGA 56
19 rPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProSerGlu 36
|||||
57 GTACAGCATTAATCCATTTGTACCAAGAGGCGTATACCCACGACAAG 106
36 hrPheThrArgValGlnLysTyrGlyLeuThrLeuValThrThrAsp 52
|||||
107 ATTCGTAAACGGTGAAAAAGTACGATCTTACGTTACTAAAGACACATGAT 156
53 LeuGluLeuIleLysTyrLeuAsnValValGluGlnLysAspTrp 69
|||||
157 GATGAACGTGAAGATACATTCGGAAAATCTTCTCAAGATTACAGGTG 206
69 pLeuTyrLysCysSerValGlnLysLeuValValIleSerAsnIleG 86
|||||
207 GCTTCCTTGGTGGAAAATGCAATCAATAGTATTATGTTAGTACACAAG 256
86 luSerGlyGluValLeuGluArgTrpGlnPheAspIleGlu..... 99
|||||
257 ATGAGGAGAGGAGTGGTGGAAAAGATGGTCTTCAATGTGCAACACATTCT 306
100 CysAspLysThrAlaLysAspAspSerAlaProArgGluLysSerGlnLy 116
|||||
307 GGCAATAGCAACGGGCGAGGATGATGTTGTA.....GATTAAA 344
116 sAlaIleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrV 133
|||||
345 TACAACACATCAATCAATCAGAGCTTTAATCAGGCAATACCTCAACCG 394
133 alThrPheLeuProLeuLeu.....GluValSerCysSerPheAspLeu 147
|||||
395 TTACCTTTCTGCCGGAATAACAAAGAGGTGGGTACACATTCACAGTA 444
148 LeuIleTyrThrAspLysAspLeuValValProGluLysTrpGluGluSe 164
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445 CTTGCATATACAGACGGGATGCTAAAGTTCCGTTAAGATGGCGGACTC 494
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495 CAATAGTAAGAGATACCTGATGCTGGAAGTAGTTCAATTCAAACATTCT 544
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seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-09-145-868-4

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seq_documentation_block:
: Sequence 4, Application US/09145868
: Patent No. 6096522
: GENERAL INFORMATION:
: APPLICANT: Benezia, Robert
: TITLE OF INVENTION: GENE ENCODING THE HUMAN HOMOLOG OF MAD2
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/145,868
: FILING DATE: 02-SEP-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 1747/46621-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0526
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 591 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: PS-09-145-868-4

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alignment_scores:
  Quality: 395.50      Length: 197
  Ratio: 2.637         Gaps: 3
  Percent Similarity: 76.142  Percent Identity: 43.147

alignment_block:
  US-09-352-570-2 x US-09-145-868-4 ..

  Alignment seg 1/1 to: US-09-145-868-4 from: 1 to: 591

3  GlnGlyIleThrLeuArgGlySerAlaGluIleValAlaGluPhePhe 19
7  CAATCATATCACTAAGGGTTCAACAGGACAGTTTACAGAATTTTCGA 56
19  rPheGlyIleAsnSerIleLeuTyrGlnArgGlyIleTyrProSerGluT 36
57  GTACAGCATTAATTCATTTTGTACCAAAAGAGCGGTATACCCAGCAGAG 106
36  hrPheThrArgValGlnLysTyrGlyLeuThrLeuLeuValThrThrAsp 52
107  ATTTTCGTAACGGTGAAGAAAGTACGATCTTACGTTACTAAAGACACATGAT 156
53  LeuGlnLeuIleLysTyrLeuAsnAsnValGluGlnLeuLeuLysAspTr 59
157  GATGAAGTGAAGATTACATTTCGGAATAATCTTCTCAAGTTTCACAGGTG 206
69  pLeuTyrLysCysSerValGlnIlysIleuValValIleSerAsnIleG 86
207  GCCTCTTGGTGAAGATGCAATTAAGTATGATTTATGATTTATGACAGG 256

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Quality: 72.50 Length: 171
Ratio: 0.797 Gaps: 8
Percent Similarity: 53.216 Percent Identity: 19.883

- alignment_block:

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833 AAGGTCTCTATCTCAGAGCTGTAAACAGCCCTCAGGTAATACGGA 882
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45 uThrLeuValThrThrAspLeuGluLeuLysTyr..... 58
   ||| :::::
883 GACAAATAACCTTAAACCGCTATTGACGCTTAAACGTTGATAAAACGT 932
   ||| :::::
59 ..LeuAsnAsnValValGluGlnLeuLysAspTrpLeuTyrLysCysSer 74
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933 AATTAAACAATACGATTGACAGTGCACAAA..... 961
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75 ValGlnLysLeuValValValIleSerAsnIleGluSerGlyGluVal 91
   :::::
962 .....ACAAAGGTAAAGAACATTACAGTGA 987
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91 uGluArgTTPGlnPheAspIleGluCysAspLysThrAlaLysAspAsp 108
   :::::
988 TAGAAGTTGCGAA...AACTCCAACTGAAGTTACAAAGGCGTGAAGAG 1034
   ||| :::::
108 exAlaProArgGluLysSerGlnLysAlaIleGlnAspGluLysSer 124
   ||| :::::
1035 TTGCA.....GCTATACAGATGCTAAACAAAGTGAAGTTAACGAA 1075
   ||| :::::
125 ValIleArgGlnIleThrAlaThrValThrPheLeuProLeuLeuGluVa 141
   :::::
1076 GCTGTTGAAAAATTAACCTCAACTATTGAA.....AAATTGTTGAAT 1119
   ||| :::::
141 lSerCysSerPheAspLeuLeuIleTyrThrAspLysAspLeuValValp 158
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1120 ATCT...GAAAGCCCAATATTACATGTACTAGTACCGATAGAAAATAT 1166
   ||| :::::
158 roGluLysTrpGluGluSerGlyProGlnPheIleThrAsnSerGluGlu 174
   ||| :::::
1167 TGAACGT...GAAGCTGTGCTAAGTATATCTAGAAATCAAAACAAA 1213
   ||| :::::
175 ValArgLeuArgSerPheThrThrThrIleHisLys.....Va 187
   :::::
1214 ACAAATAATCAATCAATCACAGTGAATTGAAAAAAGGAGAGAAAGTTAT 1263
   ||| :::::
187 lAsnSerMetVal 191
   ||| :::::
1264 TAATACTGTAGTC 1276
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eq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-261-206A-71

-eq_documentation_block:

Sequence 71, Application US/08261206A

Patent No. 5574007

GENERAL INFORMATION:

APPLICANT: Zushi, Mitichitaka

APPLICANT: Gomi, Komakazu

APPLICANT: Yamamoto, Shuji

APPLICANT: Suzuki, Koji

APPLICANT: Matsuda, Akio

TITLE OF INVENTION: A Polypeptide Capable of Interacting

with Thrombin

NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 N. Washington St.

CITY: Falls Church

STATE: Virginia

COUNTRY: USA

ZIP: 22046-0747.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261.206A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/740,492

FILING DATE: 03-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Svensson, Leonard R.

REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 216-275P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300

TELEFAX: 703-241-2848

TELEX: 248345

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 3306 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Acremonium chrysogenum

FEATURE:

NAME/KEY: -

LOCATION: 1..3306

OTHER INFORMATION: /label= PKG_gene

OTHER INFORMATION: /note= "Nucleotide sequence of region A in Figure 59. The sequence is presented as Figure 61."

FEATURE:

NAME/KEY: exon

LOCATION: 1252..1317

FEATURE:

NAME/KEY: exon

LOCATION: 1463..1883

FEATURE:

NAME/KEY: exon

LOCATION: 1948..2715

FEATURE:

NAME/KEY: CDS

LOCATION: join(1252..1317, 1463..1883, 1948..2714)

US-08-261-206A-71

alignment_scores:

Quality: 72.50 Length: 84

Ratio: 1.480 Gaps: 3

Percent Similarity: 58.333 Percent Identity: 32.143

alignment_block:

US-09-352-570-2 x US-08-261-206A-71 ..

Align seg 1/1 to: US-08-261-206A-71 from: 1 to: 3306

42 LysTyrGlyLeuThrLeuValThrThrAspLeuGluLeuLysTyr 58

||||| ::::: |||

1619 AAGTACTCGCTGCAGCCCGTGTCCCC.....GAGCTCGAGAGCT 1659

||||| ::::: |||

58 rLeuAsnAsnValValGluGlnLeuLysAspTrpLeuTyrLysCysSerV 75

||||| ::::: |||

1660 GCTCGGCAAGAGCGTCACTTTCCGCCCGCAC.....TCGCTCG 1697

||||| ::::: |||

75 aGlnLysLeuValValIleSerAsnIleGluSerGlyGluVal... 90

||||| ::::: |||

1698 GCGCGAGGTGAGGGCTTCGTCCGCAAGCGGCGCGCGTGTTC 1747

```
91 ...LeuGluArgTrpGlnPheAspIleGluCysAspLysThrAlaLysAs 106
|||||...:|||||...:|||||...:|||||...:|||||...:
1748 CTCTCGAGAACCTCCGCTCCATCGAGGAGGAGGAGGCCCAAGGA 1797
106 pAspSerAlaProArgLysSerGlnLysAlaIleGlnAspGluIleA 123
|:|||||...:|||||...:|||||...:|||||...:|||||...:
1798 TAAGGATGGAACAAGCAAGCAAGCTGACAAAGGCGCAAAAGTTGACGAGTCC 1847
123 rg 123
1848 GC 1849
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-139-424-3

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seq_documentation_block:
; Sequence 3, Application US/09139424
; Patent No. 5985832
GENERAL INFORMATION:
APPLICANT: Roodman, G. David
APPLICANT: Reddy, Sakamuri V.
APPLICANT: Choi, Sun-Jin
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE FOR
TITLE OF INVENTION: OSTEOCLAST INHIBITORY FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,424
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/772,441
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSK:295
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1936 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1434
JS-09-139-424-3

alignment_scores:
Quality: 72.00 Length: 125
Ratio: 0.986 Gaps: 8
Percent Similarity: 58.400 Percent Identity: 29.600

alignment_block:
JS-09-352-570-2 x US-09-139-424-3
Align seg 1/1 to: US-09-139-424-3 from: 1 to: 1936
7 LeuArgGlySerAlaGluIleValAlaGluPheSerPheGlyIleAs 23
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|||||...:|||||...:|||||...:|||||...:|||||...:
484 TTGAGAGCGGATCGACAGACCACTGAAG.....GGCATAGGATCCGG 524
23 nSerIleLeuTyrGlnArgGly.....IleTyrProS 34
:|||||...:|||||...:|||||...:|||||...:|||||...:
525 CAAAGTCCCTG...AAGAGTGGCCCCCAGGATCACGTGTTCATTAC.... 567
34 erGluThrPheThrArgValGlnLysTyrGlyLeuThrLeuLeuValThr 50
|||||...:|||||...:|||||...:|||||...:|||||...:
568 .....TTCACTGACCATGGATCTACTGGAATACTGGTTTTTCCCAAT 609
51 ThrAspLeuGluLeuIleLysTyrLeuAsnAsnValValGluGlnLeuL 67
|||||...:|||||...:|||||...:|||||...:|||||...:
610 GAAGATCTTCAT...GTAAGGACCTGGAATGAGACCATCCAT..... 648
67 sAspTrpLeuTyrLysCysSerVal...GlnLysLeuValValIleS 83
:|||||...:|||||...:|||||...:|||||...:|||||...:
649 ...TACATGTACAAACACAAAATGTACCGAAAGATGGTGTCTACATTG 694
83 erAsnIleGluSerGlyGluValLeuGluArgTrpGlnPheAspIleGlu 99
:|||||...:|||||...:|||||...:|||||...:|||||...:
695 AAGCCTGTGAGTCTGGTCCATGATGACCACTGCGCGGATACATCAAT 744
100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLy 116
|||||...:|||||...:|||||...:|||||...:|||||...:
745 GTTATGCAACTACTGCT.....GCCAACCCAGAGAGTCTGCTCTACGC 788
116 sAlaIleGlnAspGluIleArgSer 124
:|||||...:|||||...:|||||...:|||||...:|||||...:
789 CTGTTACTATGATGAGAGAGGTCC 813
seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-706-216-3

seq_documentation_block:
; Sequence 3, Application US/08706216
; Patent No. 6140098
GENERAL INFORMATION:
APPLICANT: Balasubramanian, Sriam
APPLICANT: Ford, John
APPLICANT: Gorman, Daniel M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MAMMALIAN PROTEASES; RELATED REAGENTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,216
FILING DATE: 30-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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FEATURE:
NAME/KEY: CDS
LOCATION: 183..1484
S-08-706-216-3

alignment_scores:
Quality: 72.00 Length: 135
Ratio: 0.986 Gaps: 8
Percent Similarity: 58.400 Percent Identity: 29.600

alignment_block:
US-09-352-570-2 x US-08-706-216-3 ..

Align seg 1/1 to: US-08-706-216-3 from: 1 to: 2030

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|||||
531 TTGAGAGCGGATGCGAGAGCAGTGAAG.....GGCATAGGATCCGG 571
23 nSerIleuTyrglnArgGly.....IleTyrglnPro 34
: : : : :
572 CAAAGCTCTG...AAGAGTGGCCGCCAGGATCAGCTGTTCATTAC.... 614
34 erGluThrPheThrArgValGlnLysTyrglyLeuThrLeuValThr 50
||||| : : : : :
615TTCACCTGACCATGATCTACTGGAATACGTGTTTCCCAAT 656

51 ThrAspLeuGluLeuIleLysTyrglyLeuAsnValValGluGlnLeu 67
||||| : : : : :
657 GAAGATCTTCAT...GTAAGACCTGATGAGACCATCCAT..... 695

67 sasTrpLeuTyrglySerVal....GlnLysLeuValValIleAs 83
: : : : :
696TACATGTACAAACAAATGATCCGAAAGATGGTGTCTCATTTG 741

83 erAsnIleGluSerGlyGluValLeuGluArgTrpGlnPheAspLeu 99
: : : : :
742 AAGCTGTGAGTCTGGTCCATGATGACCACTCCCGGATAACATCAAT 791

100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGln 116
: : : : :
792 GTTATGCACTACTGCT.....GCCAACCCAGAGAGTCTCTACGC 835

116 salaIleGlnAspGluIleArgSer 124
: : : : :
836 CTGTTACTATGATGAGAAGAGTCC 860

eq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-206-176-5

eq_documentation_block:
Sequence 5, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dairymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
TITLE OF INVENTION: Animals
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: human fibrinogen gamma chain
FEATURE:
NAME/KEY: CDS
LOCATION: Join(1799..1876, 1973..2017, 2207..2390, 2510
LOCATION: ..2603, 4211..4341, 4645..4778, 5758..5942, 7426
LOCATION: ..7703, 9342..9571)
US-08-206-176-5

alignment_scores:
Quality: 72.00 Length: 98
Ratio: 1.220 Gaps: 4
Percent Similarity: 60.204 Percent Identity: 25.510

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Align seg 1/1 to: US-08-206-176-5 from: 1 to: 10564

13 IleValAlaGluPheSerPheGlyIleAsnSerIleLeuTyrglnAr 29
: : : : :
4047 TTGTAATATAATTTTACATTTTCTCAAGAATGGAATAATTTATCAGAA 4096

29 gGlyIleTyrglnProSerGluThrPheThrArgValGlnLysTyrglyLeu 46
: : : : :
4097 AGCACTCTTAAAGAAATACCTACGAGTTTCCAAAGAAATATAAATA 4146

46 hrLeu.....LeuValThrAspLeuGluLeuIleLysTyrg 58
||||| : : : : :
4147 CTCCTCTGAAAGGAATACCTATTTTCTCTTATTTTCTTATCTAT 4196

59 LeuAsnValValGluGlnLeuLysAspTrpLeuTyrglyLysCysSerVa 75
: : : : :
4197 GTT...TCTGTTTGTAGATATTTCCAGAA...ATATATAATTCAAATAA 4240

75 gLysLeuValValIleSerAsnIleGluSerGlyGluValLeuG 92
||||| : : : : :
4241 TCAAAAGATTTTAACTGAAGAGAGAGAGTAGCC..... 4274

92 luArgTrpGlnPheAspIleGluCysAspLysThrAlaLysAsp 106
: : : : :
4275CAGCTTGAAGCACAGTGCAGGAGACCTTGCAAGAC 4310

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-568-147B-1

seq_documentation_block:
Sequence 1, Application US/08568147B
Patent No. 5783422
GENERAL INFORMATION:
APPLICANT: Suminami, Yoshinori
APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Katsumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL


```
68 pTrpLeuTyrLysCysSerValGlnLysLeuValValValIleSerAsnI 85
1925 .....AAATGTAATAAAGATAGTTCCTCGTGGATG 1886
85 leGluSerGlyGluValLeuGluArg.....TrpGlnPheAspIleGlu 99
1885 TTAGAAATAAAGTACTTTGACGAAGCGCTAGATCAGCAGATGTGTC 1836
100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLy 116
1835 ATTCATATTGCTTCGATAAATGATGACG.....GGTAA 1801
116 salalleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrV 133
1800 GTTACTAACGACTCTATAATGGACGT.....AATATCAACGAACGA 1757
133 alThrPheLeuProLeuLeuGluValSerCysSerPheAsp..... 146
1756 AGAAGCTAGTAGAT.....TCTTCTCTGTATACGGCGTAAGA 1719
147 LeuLeuIleTyrThrAspLysAspLeuValValProGluLysTrpGluG 163
1718 GTCTTAGTATATAGC.....AGTAGTTATTCTGTC 1690
163 uSerGlyProGlnPheIleThrAsnSerGluGluValValArgLeuArgSerP 180
1699 GGTAGTCCTAACCTTCTCCGGAGATGCGATGAAGAGAAACGAGAAT 1640
180 heThrThrThrIle 184
1639 ACGTATTATCAATC 1626
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seq_documentation_block:
: Sequence 75, Application US/08220151
: Patent No. 5525780
: GENERAL INFORMATION:
: APPLICANT: Paoletti, Enzo
: APPLICANT: Limbach, Keith J.
: TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
: TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
: NUMBER OF SEQUENCES: 91
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Curtis, Morris & Safford
: STREET: 530 Fifth Avenue
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/220,151
: FILING DATE: 30-MAR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Frommer, William S.
: REGISTRATION NUMBER: 25,506
: REFERENCE/DOCKET NUMBER: 454310-2540
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 840-3333
: TELEFAX: (212) 840-0712
: TELEX: 425066 CURTMS
: INFORMATION FOR SEQ ID NO: 75:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2356 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-220-151-75

alignment_scores:
Quality: 71.00 Length: 138
Ratio: 0.887 Gaps: 7
Percent Similarity: 57.971 Percent Identity: 22.464

alignment_block:
US-09-352-570-2 x US-08-220-151-75/rev ..
Align seg 1/1 to reverse of: US-08-220-151-75 from: 1 to: 2356

52 AspLeuGluLeuIleLysTyrLeuAsnValValGluGlnLeuLysAs 68
1964 GATATTAGAATCGACCAATGTTACTAGATCTTGTAGAA..... 1926
68 pTrpLeuTyrLysCysSerValGlnLysLeuValValValIleSerAsnI 85
1925 .....AAATGTAATAAAGATAGTTCCTCGTGGATGCGATG 1886
85 leGluSerGlyGluValLeuGluArg.....TrpGlnPheAspIleGlu 99
1885 TTAGAAATAAAGTACTTTGACGAAGCGCTAGATCAGCAGATGTGTC 1836
100 CysAspLysThrAlaLysAspSerAlaProArgGluLysSerGlnLy 116
1835 ATTCATATTGCTTCGATAAATGATGACG.....GGTAA 1801
116 salalleGlnAspGluIleArgSerValIleArgGlnIleThrAlaThrV 133
1800 GTTACTAACGACTCTATAATGGACGT.....AATATCAACGAACGA 1757
133 alThrPheLeuProLeuLeuGluValSerCysSerPheAsp..... 146
1756 AGAAGCTAGTAGAT.....TCTTCTCTGTATACGGCGTAAGA 1719
147 LeuLeuIleTyrThrAspLysAspLeuValValProGluLysTrpGluG 163
1718 GTCTTAGTATATAGC.....AGTAGTTATTCTGTC 1690
163 uSerGlyProGlnPheIleThrAsnSerGluGluValValArgLeuArgSerP 180
1699 GGTAGTCCTAACCTTCTCCGGAGATGCGATGAAGAGAAACGAGAAT 1640
180 heThrThrThrIle 184
1639 ACGTATTATCAATC 1626
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